

TECH CENTER 1600/2900

JAN 02 2001

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/589,870B

DATE: 12/13/2001

TIME: 13:38:12

Input Set : A:\547.app.txt

Output Set: N:\CRF3\12132001\I589870B.raw

ENTERED

4 <110> APPLICANT: Goshorn, Stephen C.  
5 Graves, Scott Stoll  
6 Schultz, Joanne Elaine  
7 Lin, Yakang  
8 Sanderson, James A.  
9 Reno, Jonh M.

11 <120> TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
12 METHODS OF USE THEREOF

15 <130> FILE REFERENCE: 690022.547

17 <140> CURRENT APPLICATION NUMBER: US 09/589,870B

C--> 18 <141> CURRENT FILING DATE: 2001-11-30

20 <160> NUMBER OF SEQ ID NOS: 47

22 <170> SOFTWARE: FastSEQ for Windows Version 4.0

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 638

26 <212> TYPE: DNA

27 <213> ORGANISM: Streptomyces avidinii

29 <400> SEQUENCE: 1

30	ccctccgtcc cgcgcgggca acaactaggg agtatttttc gtgtctcaca tgcgcaagat	60
31	cgtcgttgca gccatcgccg ttcccttgac caccggtctcg attacggcca gcgcttcggc	120
32	agacccctcc aaggactcga aggccaggt ctgcggccgc gaggccggca tcaccggcac	180
33	ctggtacaac cagctcggtt cgaccttcat cgtgaccgcg ggcgcgcgac gcgccctgac	240
34	cggaaacctac gagtcggccg tcggcaacgc cgagagccgc tacgtcctga ccggtcgtta	300
35	cgacagcgcc ccggccaccg acggcagcgg caccgccttc ggttggaagg tggcctggaa	360
36	gaataactac cgcaacgccc actocgcgac cactgtggagc ggccagtacg tcggcggcgc	420
37	cgaggcgagg atcaacaccc agtggctgct gacctccggc accaccgagg ccaacgcctg	480
38	gaagtccacg ctggtcggcc acgacacctt caccaagggtg aagccgtccg ccgcctccat	540
39	cgacgcggcg aagaaggccg gcgtcaacaa cggcaaccgc ctcgacgccg ttcagcagta	600
40	gtcgcgtccc ggcaaccggc ggtgcccggg cctcggcc	638

42 <210> SEQ ID NO: 2

43 <211> LENGTH: 183

44 <212> TYPE: PRT

45 <213> ORGANISM: Streptomyces avidinii

47 <400> SEQUENCE: 2

48	Met Arg Lys Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val	
49	1 5 10 15	
50	Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala	
51	20 25 30	
52	Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln	
53	35 40 45	
54	Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala Asp Gly Ala Leu Thr	
55	50 55 60	
56	Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu Ser Arg Tyr Val Leu	
57	65 70 75 80	
58	Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp Gly Ser Gly Thr Ala	
59	85 90 95	
60	Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr Arg Asn Ala His Ser	

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61          100          105          110
62 Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly Ala Glu Ala Arg Ile
63          115          120          125
64 Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr Glu Ala Asn Ala Trp
65          130          135          140
66 Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr Lys Val Lys Pro Ser
67 145          150          155          160
68 Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly Val Asn Asn Gly Asn
69          165          170          175
70 Pro Leu Asp Ala Val Gln Gln
71          180
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 1612
75 <212> TYPE: DNA
76 <213> ORGANISM: Streptomyces avidinii
78 <400> SEQUENCE: 3
79 gaattcacga agtaaccgac aggactcggc cattctttgg ccgaaattcc tttgcagaaa      60
80 atgttggtga gaaccctccg atggctagta cgatttacac cgaacatgtg cccttggtgaa      120
81 ccatcgaccc ggacctcgac catccagttc tgccgccaaa gacacatgcc gcactgctgt      180
82 ttgttcaccg acaccgtcag gtgcacggcc gaggtcacia accttgacgg gcgggatacg      240
83 gacggcgcac gccacagcgc gccctccgtc ccgcgcgggc aacaactagg gagtattttt      300
84 cgtgtctcac atgcgcaaga tcgtcgttgc agccatcgcc gtttccttga ccacggtctc      360
85 gattacggcc atggctgaca tccagatgac tcagtctcca tcgtccttgt ctgcctctgt      420
86 gggagacaga gtcacgatca cttgtcgggc tagtcagggc attagaggta atttagactg      480
87 gtatcagcag aaacctggta agggaccgaa actcctaata tactccacat ccaatttaaa      540
88 ttctggtgtc ccatcaaggt tcagtggcag tgggtctggg tcagattata ctctcaccat      600
89 cagcagcctt cagcctgaag atttcgcaac gtattactgt ctacagcgta atgcgtatcc      660
90 gtacacgttc ggacaaggga ccaagctgga gatcaagatc tctggtggcg gtggctcggg      720
91 cgggtggtggg tcgggtggcg gaggtcagag ccaggttcag ctggtccagt ctggggcaga      780
92 ggtgaaaaag ccaggggcct cagtcaaggt gtccctgcaag gcttctggct tcaacattaa      840
93 agacacctat atgcactggg tgaggcaggc acctggacag ggctgcagt ggatgggaag      900
94 gattgatcct gogaatggtg atactaaatc cgacctgtcc ttccagggca gggtgactat      960
95 aacagcagac acgtccatca acacagccta catggaactc agcagcctga ggtctgacga      1020
96 cactgccgtc tattactgtt ctagagaggt cctaactggg acgtggctct tggactactg      1080
97 gggccaagga accttagtca ccgtgagctc tggctctggg tcggcagacc cctccaagga      1140
98 ctccaaggcc caggtctcgg ccgccaggc cgccatcacc ggcacctgtt acaaccagct      1200
99 cggctcgacc ttcacgtgta ccgcgggcgc cgacggcgcc ctgaccggaa cctacgagtc      1260
100 ggccgtcggc aacgccgaga gccgctacgt cctgaccggt cgttacgaca gcgccccggc      1320
101 caccgacggc agcggcaccg ccctcggttg gacggtggcc tggaagaata actaccgcaa      1380
102 cgcccaactcc gcgaccacgt ggagcggcca gtacgtcggc ggcgccgagg cgaggatcaa      1440
103 caccagtggt ctgctgacct ccggcaccac cgaggccaac gcctggaagt ccacgtggt      1500
104 cgccacagac accttcacca aggtgaagcc gtccgccgcc tccatcgacg cggcgaagaa      1560
105 ggccggcgtc aacaacggca acccgctcga cgccgttcag cagtaaggat cc      1612
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 431
109 <212> TYPE: PRT
110 <213> ORGANISM: Streptomyces avidinii
112 <400> SEQUENCE: 4
113 Met Arg Lys Ile Val Val Ala Ala Ile Ala Val Ser Leu Thr Thr Val

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114 1          5          10          15
115 Ser Ile Thr Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
116          20          25          30
117 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
118          35          40          45
119 Gln Gly Ile Arg Gly Asn Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys
120          50          55          60
121 Gly Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val
122 65          70          75          80
123 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr
124          85          90          95
125 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
126          100          105          110
127 Arg Asn Ala Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
128          115          120          125
129 Lys Ile Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
130          130          135          140
131 Gly Ser Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
132 145          150          155          160
133 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
134          165          170          175
135 Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
136          180          185          190
137 Gln Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Ser Asp
138          195          200          205
139 Leu Ser Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn
140          210          215          220
141 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val
142 225          230          235          240
143 Tyr Tyr Cys Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr
144          245          250          255
145 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Ala
146          260          265          270
147 Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly
148          275          280          285
149 Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr
150          290          295          300
151 Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly
152 305          310          315          320
153 Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro
154          325          330          335
155 Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys
156          340          345          350
157 Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr
158          355          360          365
159 Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser
160          370          375          380
161 Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp
162 385          390          395          400

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163 Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys
164          405          410          415
165 Lys Ala Gly Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln
166          420          425          430
168 <210> SEQ ID NO: 5
169 <211> LENGTH: 1239
170 <212> TYPE: DNA
171 <213> ORGANISM: Streptomyces avidinii
173 <400> SEQUENCE: 5
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175 atgacttgca gggccagctc aagtgtaatg tacatgcact ggtaccagca gaagccagga      120
176 tcctccccc aaccctggat ttatgccaca tccaacctgg ctctctggagt ccctgctcgc      180
177 ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagagt ggaggctgaa      240
178 gatgctgcca cttattactg ccagcagtggt attagtaacc caccacggtt cgggtgctggg      300
179 accaagctgg agctgaagat ctctggtctg gaaggcagcc cggaagcagg tctgtctctcg      360
180 gacgcaggtt ccggctcgag ccaggttcag ctggtccagt caggggctga gctggtgaag      420
181 cctggggcct cagtgaagat gtctcgcaag gcttctggct acacatttac cagttacaat      480
182 atgcactggg taaagcagac acctggacag ggctggaat ggattggagc tatttatcca      540
183 ggaaatggtg atacttccta caatcagaag ttcaaaggca aggccacatt gactgcagac      600
184 aaatcctcca gcacagccta catgcagctc agcagcctga catctgagga ctctgcggtc      660
185 tattactgtg caagagcgca attacgacct aactactggt acttcgatgt ctggggcgca      720
186 gggaccacgg tcaccgtgag ctctggtctt ggttcggcag acccctccaa ggactcgaag      780
187 gccaggtctc cggccgcgga ggccggcacc accggcacct ggtacaacca gctcggctcg      840
188 accttcacg tgaccgcggg cgccgacggc gccctgaccg gaacctacga gtcggccgctc      900
189 ggcaacgccc agagccgcta cgtcctgacc ggtcgttacg acagcgcccc ggccaccgac      960
190 ggcagcgcca ccgccctcgg ttggacggtg gcctggaaga ataactaccg caacgcccac     1020
191 tccgcgacca cgtggagcgg ccagtagctc ggcggcgccg aggcgaggat caacaccacg     1080
192 tggctgctga cctccggcac caccgaggcc aacgcctgga agtcacgct ggtcggccac     1140
193 gacaccttca ccaaggtgaa gccgtccgcc gcctccatcg acgcggcgaa gaaggccggc     1200
194 gtcaacaacg gcaacccgct cgacgccgtt cagcagtaa      1239
196 <210> SEQ ID NO: 6
197 <211> LENGTH: 412
198 <212> TYPE: PRT
199 <213> ORGANISM: Streptomyces avidinii
201 <400> SEQUENCE: 6
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203 1          5          10          15
204 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
205          20          25          30
206 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
207          35          40          45
208 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
209          50          55          60
210 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
211 65          70          75          80
212 Asp Ala Ala Thr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr
213          85          90          95
214 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ile Ser Gly Leu Glu Gly
215          100          105          110

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216 Ser Pro Glu Ala Gly Leu Ser Pro Asp Ala Gly Ser Gly Ser Ser Gln
217      115      120      125
218 Val Gln Leu Val Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
219      130      135      140
220 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn
221 145      150      155      160
222 Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly
223      165      170      175
224 Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys
225      180      185      190
226 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
227      195      200      205
228 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
229      210      215      220
230 Arg Ala Gln Leu Arg Pro Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala
231 225      230      235      240
232 Gly Thr Thr Val Thr Val Ser Ser Gly Ser Gly Ser Ala Asp Pro Ser
233      245      250      255
234 Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly
235      260      265      270
236 Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala
237      275      280      285
238 Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu
239      290      295      300
240 Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp
241 305      310      315      320
242 Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr
243      325      330      335
244 Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly
245      340      345      350
246 Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr
247      355      360      365
248 Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr
249      370      375      380
250 Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly
251 385      390      395      400
252 Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln
253      405      410

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255 &lt;210&gt; SEQ ID NO: 7

256 &lt;211&gt; LENGTH: 1280

257 &lt;212&gt; TYPE: DNA

258 &lt;213&gt; ORGANISM: Streptomyces avidinii

260 &lt;400&gt; SEQUENCE: 7

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262 tgaagatgtc ctgcaaggct tctggctaca catttaccag ttacaatatg cactgggtaa      120
263 agcagacacc tggacagggc ctggaatgga ttggagctat ttatccagga aatggtgata      180
264 cttcctacaa tcagaagttc aaaggcaagg ccacattgac tgcagacaaa tcctccagca      240
265 cagcctacat gcagctcagc agcctgacat ctgaggactc tgcggtctat tactgtgcaa      300
266 gagcgcaatt acgacctaac tactggtact tcgatgtctg gggcgaggg accacggtca      360

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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date